PEAK AREA



FILE NAME: SY-12

CREATED: 14:29 01-01-22
DATA: ORIGINAL

MEASURING MODE: ABS.
SCAN SPEED: FAST
SLIT WIDTH: 1.0
SAMPLING INTERVAL: 0.2

RESULT - (AREA-FACTOR) DIVISOR FACTOR = 9.999

REGIUM START END DIVISOR AREA RESULT

F I G. 1

CAMAG ILC Evaluation Software
**********************************************

ARBRO PHARMACEUTICALS LTD 6/14 KIRTI NAGAR INDUSTRIAL AREA NEW DELHI
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TLC/HPTLC-Integration (CATS3.18 S/N:0207A004 / SCANNER I I V3.14 S/N:990602)

ESTIMATION OF L-LYSINE BY HPTLC

| Calibr. Table | Calibration Table created: | ARBRO PHARMA LTD | | |
| File name: AMINO | 3/JUN/ 0 | 14:49:46 | |
| Scan | User name while measuring : | ARBRO PHARMA LTD | |
| File name: AMINO | 3/JUN/ 0 | 14:54:52 | |
| INTEGRATION | User while integrating: | ARBRO PHARMA LTD | |
| File name: AMINO | 3/JUN/ 0 | 15:19:26 | |

Track 1. Analysis a:

| Peak | start | | max | | | end | | area | |
| # | mm | h | mm | h | [%] | mm | h | a | [%] |
| 1 | 61.1 | 0.4 | 72.6 | 64.1 | 100.00 | 78.2 | 0.1 | 3186.2 | 100.00 |
| | Total height = | | | 64.1 | | Total area = | | 3186.2 | |

Track 2. Standard level 1:

| Peak | start | | max | | | end | | area | |
| # | mm | h | mm | h | [%] | mm | h | a | [%] |
| 1 | 62.9 | 2.8 | 71.0 | 63.5 | 100.00 | 78.8 | 0.0 | 3133.9 | 100.00 |
| | Total height = | | | 63.5 | | Total area = | | 3133.9 | |

F I G. 2A

CALIBRATION : H : AMINO     ARBRO PHARMA LTD     3/JUN/2000  15:05
METHOD   SCAN  [INTEGRATION]  CALIBRATION   DATA   END          HELP

STANDARD LEVEL  1

[ mV ]



WAVELENGTH: 254 nm                                      [ mm ]

TRACK:  2,  NOISE LEVEL:  0.108mV,  RAW DATA FILE: AMINO
   CATS3.18 S/N: 0207A004    CAMAG SOFTWARE (c) 1996     SCANNER II: 990602

TRACK  2.   STANDARD LEVEL 1

| PEAK | START | | MAX | | | END | | AREA | |
|---|---|---|---|---|---|---|---|---|---|
| # | mm | h | mm | h | [%] | mm | h | a | [%] |
| 1 | 62.9 | 2.8 | 71.0 | 63.5 | 100.00 | 78.8 | 0.0 | 3133.9 | 100.00 |
| | TOTAL HEIGHT = 63.5 | | | | | TOTAL AREA = 3133.9 | | | |

# F I G. 2b

CALIBRATION : H : AMINO        ARBRO PHARMA LTD        3/JUN/2000  15:10
METHOD   SCAN  [INTEGRATION]  CALIBRATION   DATA   END                    HELP

STANDARD LEVEL   1



WAVELENGTH: 254 nm                                                         [ mm ]
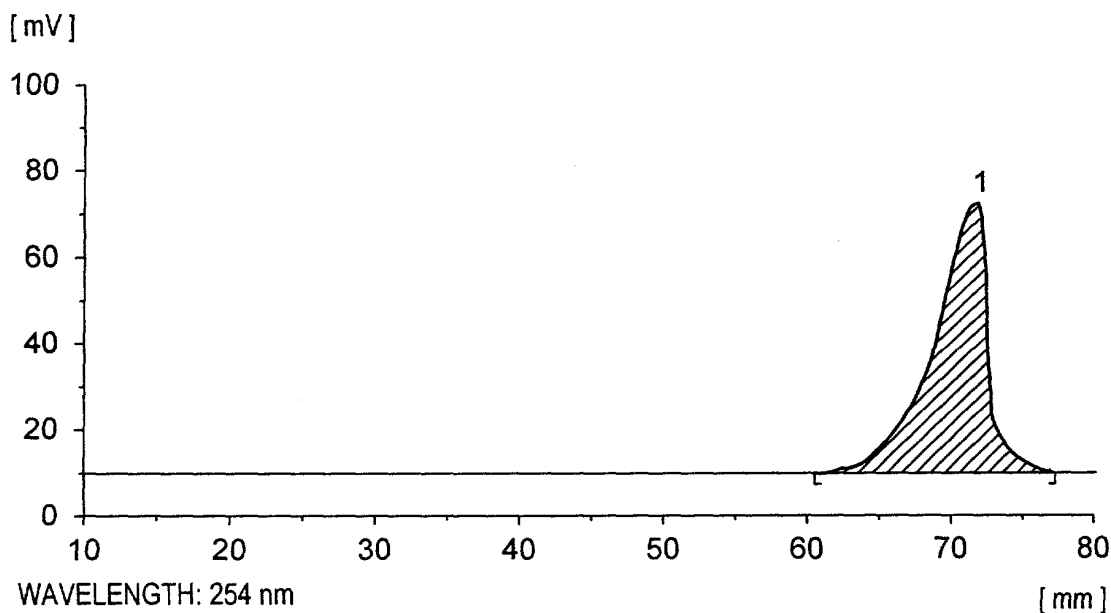
TRACK:  1, NOISE LEVEL:  0.108mV,  RAW DATA FILE: AMINO
   CATS3.18  S/N: 0207A004    CAMAG SOFTWARE (c) 1996       SCANNER II: 990602

TRACK  1.  ANALYSIS  a:

| PEAK | START | | MAX | | | END | | AREA | |
| # | mm | h | mm | h | [%] | mm | h | a | [%] |
| 1 | 61.1 | 0.4 | 72.6 | 64.1 | 100.00 | 78.2 | 01 | 3186.2 | 100.00 |
| | | | TOTAL HEIGHT = 64.1 | | | | TOTAL AREA = 3186.2 | | |

F I G. 2c

CALIBRATION : H : AMINO    ARBRO PHARMA LTD    3/JUN/2000 15:20
METHOD  SCAN [INTEGRATION] CALIBRATION  DATA  END    HELP

STANDARD LEVEL  1

100

80

60

1
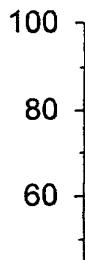
CALIBRATION : H : AMINO    ARBRO PHARMA LTD    3/JUN/2000 15:32
METHOD  SCAN [INTEGRATION] CALIBRATION  DATA  END    HELP
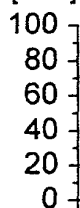
[ mV ]
100
80
60
40
20
0
10    20    30    40    50    60    70    80
WAVELENGTH: 254 nm                     [ mm ]

FILE NAME : AMINO      TRACK   1 TO 2
   CATS3.18  S/N: 0207A004   CAMAG SOFTWARE (c) 1996    SCANNER II: 990602

F I G. 2d

SUBMITTER:   PUSHPA KHANNA

SAMPLE NAME:   GOURDIN                              DATE:

| | Cycle 1 | Cycle 2 | Cycle 3 | Cycle 4 | Cycle 5 | Cycle 6 | Cycle 7 | Cycle 8 | Cycle 9 |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | HIS |
| | ASP | LEU | | | | TYR | | SER | ARG |
| | | VAL | SER | GLN | GLN | VAL | GLY — | GLN — | GLN |
| SEQUENCE: | GLY — | ILE — | GLU — | GLU — | THR — | THR ╱ | | THR | LEU |
| CYCLE #: | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |

| | Cycle 10 | Cycle 11 | Cycle 12 | Cycle 13 | Cycle 14 | Cycle 15 | Cycle 16 | Cycle 17 | Cycle 18 |
|---|---|---|---|---|---|---|---|---|---|
| | | | ARG | | | | GLY | | |
| | | TYR | HIS | HIS | | ARG | ASP | ARG | ARG |
| | LYS | ILE | ALA | GLU | ASN | MET | ASN | THR | HIS |
| SEQUENCE: | ARG — | LEU — | LYS — | TYR — | ASP — | ILE — | LEU — | ASP — | ALA |
| CYCLE #: | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |

| | Cycle 19 | Cycle 20 | Cycle 21 | Cycle 22 | Cycle 23 | Cycle 24 | Cycle 25 | Cycle 26 | Cycle 27 |
|---|---|---|---|---|---|---|---|---|---|
| | SER | | | | | | | PRO | |
| | GLU | | SER | | GLU | | THR | ARG | HIS |
| | LEU | ARG | PRO | ILE | LEU | PHE | SER | ALA | ARG |
| SEQUENCE: | LYS — | GLU — | ALA — | ASP — | ILE — | TYR — | ASN — | HIS — | GLY |
| CYCLE #: | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |

| | Cycle 28 | Cycle 29 | Cycle 30 | Cycle 31 | Cycle 32 | Cycle 33 | Cycle 34 | Cycle 35 |
|---|---|---|---|---|---|---|---|---|
| | GLY | | | VAL | | PRO | | |
| | VAL | | | LEU | ASN | ILE | ALA | |
| SEQUENCE: | ALA — | GLY — | ARG — | ILE — | SER — | THR — | VAL — | ASN |
| CYCLE #: | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 |

YIELD(pmol):   ILE(2)          98.11          YIELD(pmol):   GLU(3)      56.13

CARRYOVER:   ILE(6)          22.6%          REP YIELD:      ILE(2.23)    92.3%

SEQSTD YIELD: NL(6)          2.30   SEQSTD CARRYOVER:   NL(6)      23.0%

SEQSTD REP YIELD:      NL(6.11)   97.0%

COMMENTS:   Mixtures with interchangeable amino acid at
positions 12,13,15-19, 25-27 and 31-34.
Appears to be a mixture of sequences.

# F I G. 3a
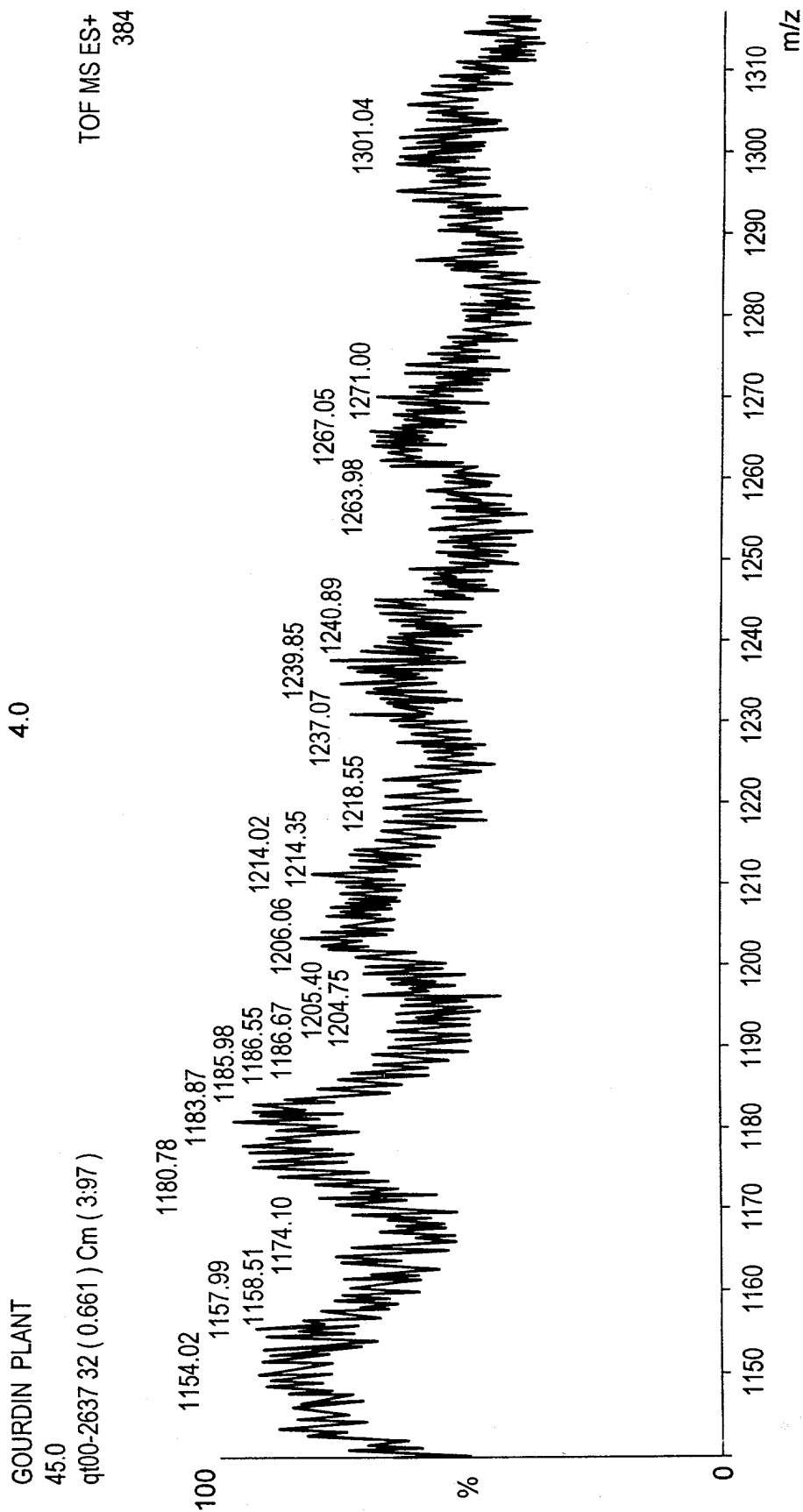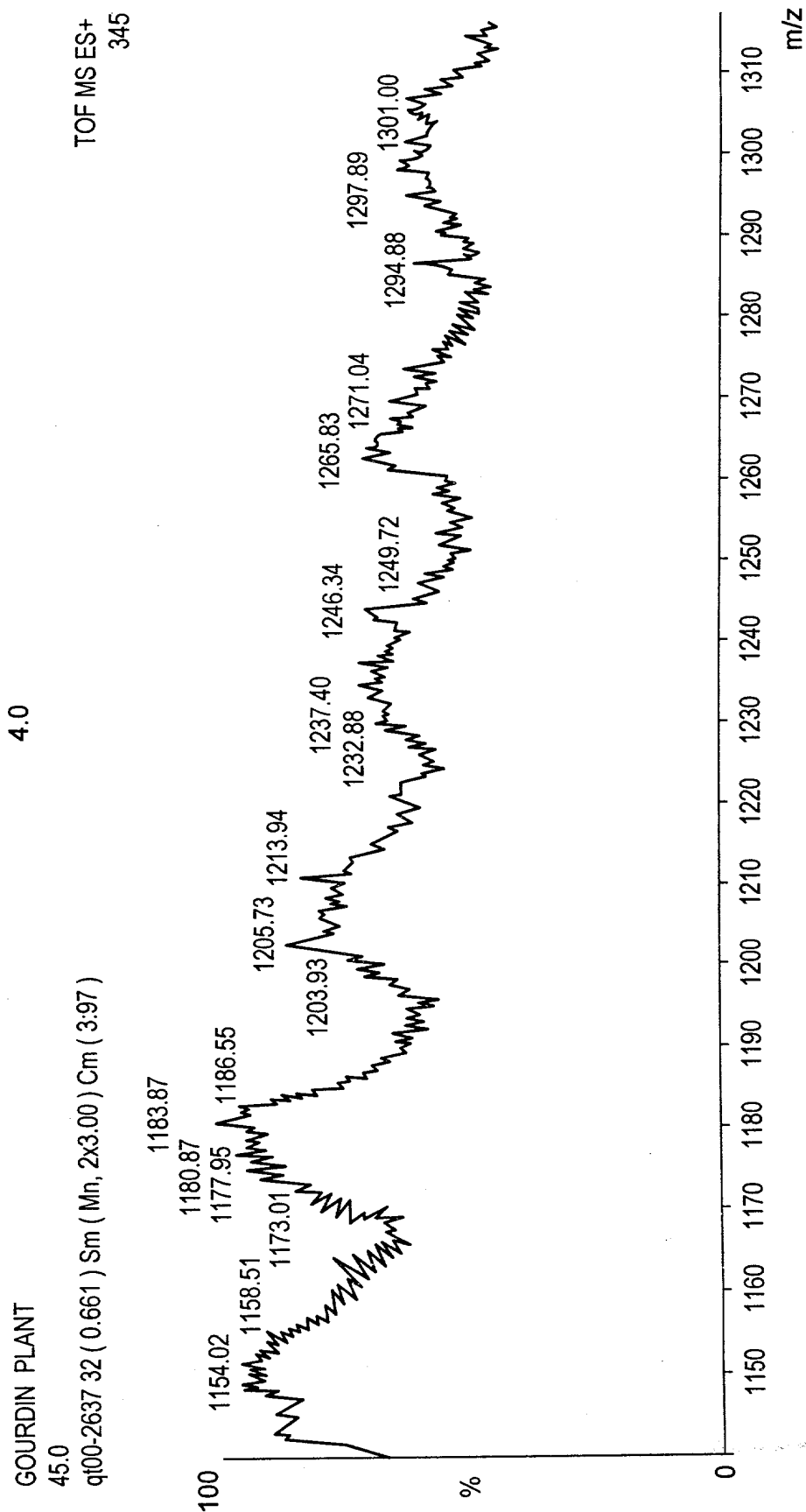
F I G. 4a1

F I G. 4a2

FIG. 4b1

GOURDIN PLANT
45.0
qt00-2637 32 ( 0.661 ) Sm (Mn, 2x3.00); Cm ( 3:97 )
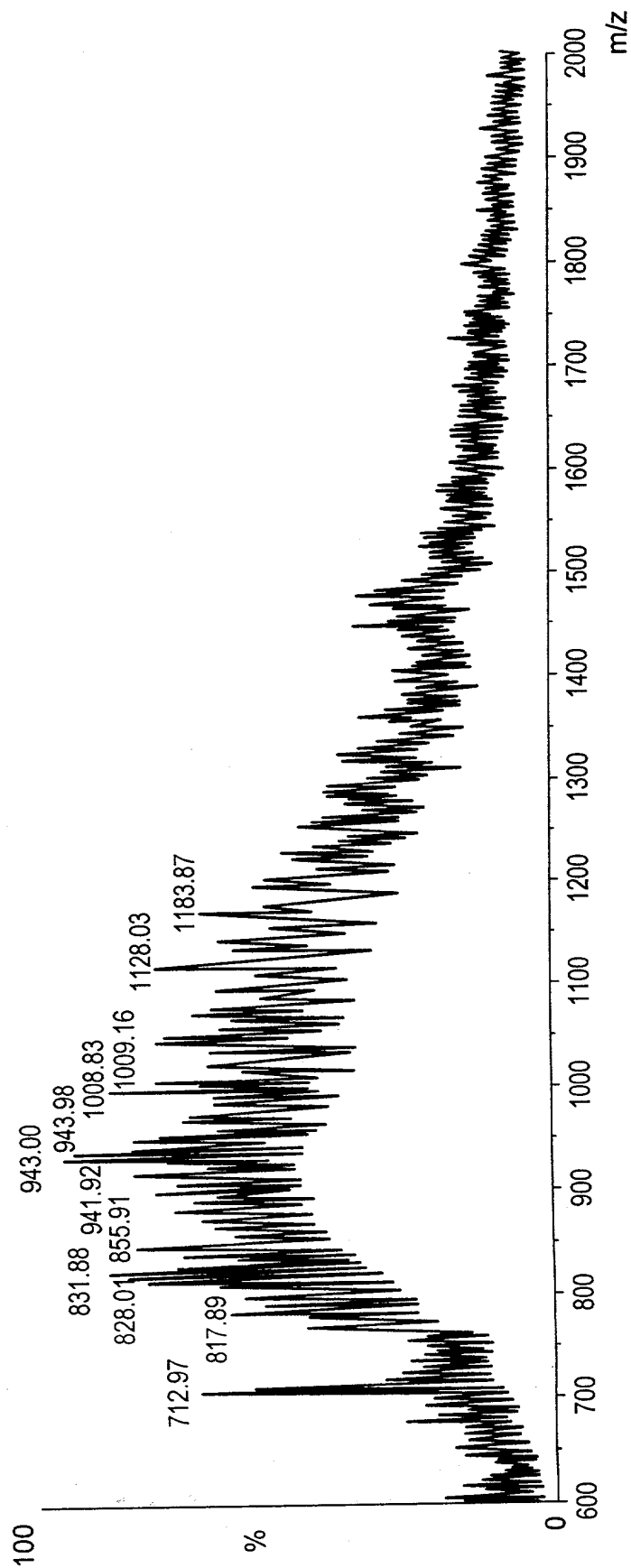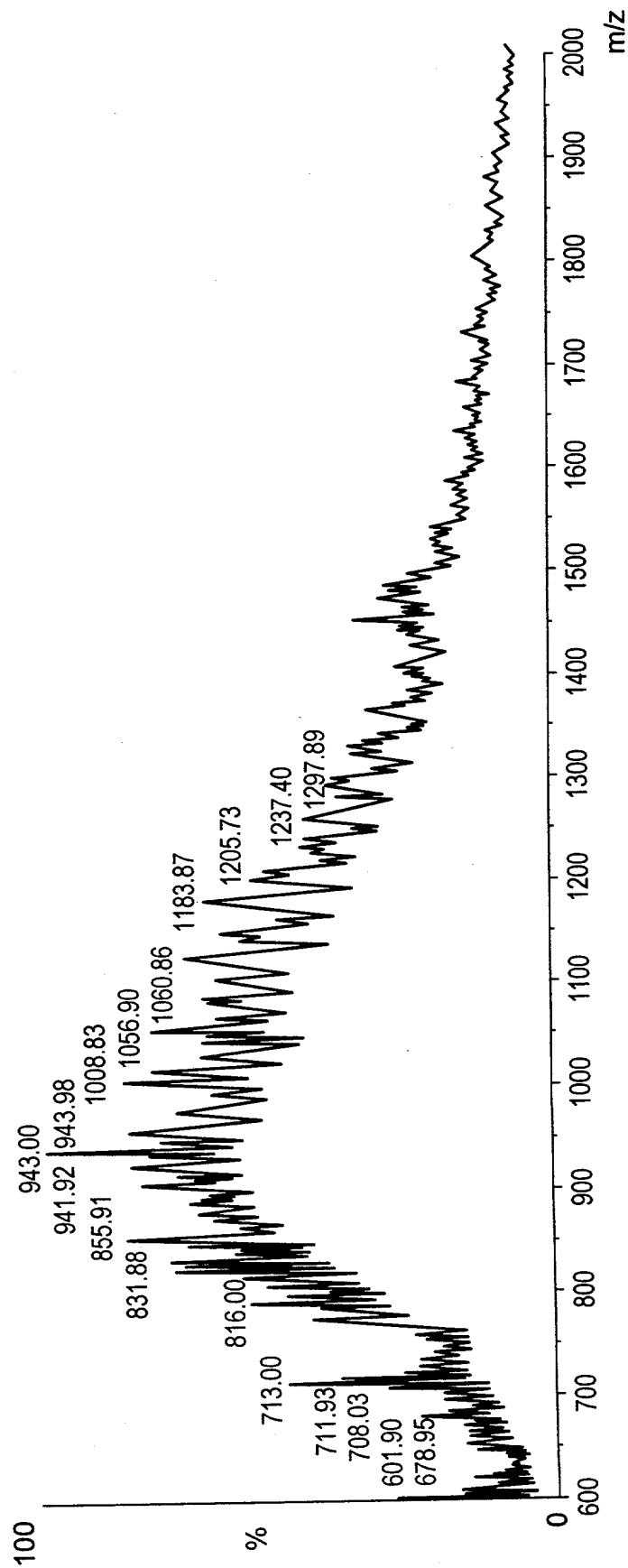
TOF MS ES+
501

4.0

F I G. 4b2

FIG. 4c

TOF MS ES+
150

FIG. 4d

F I G. 4e
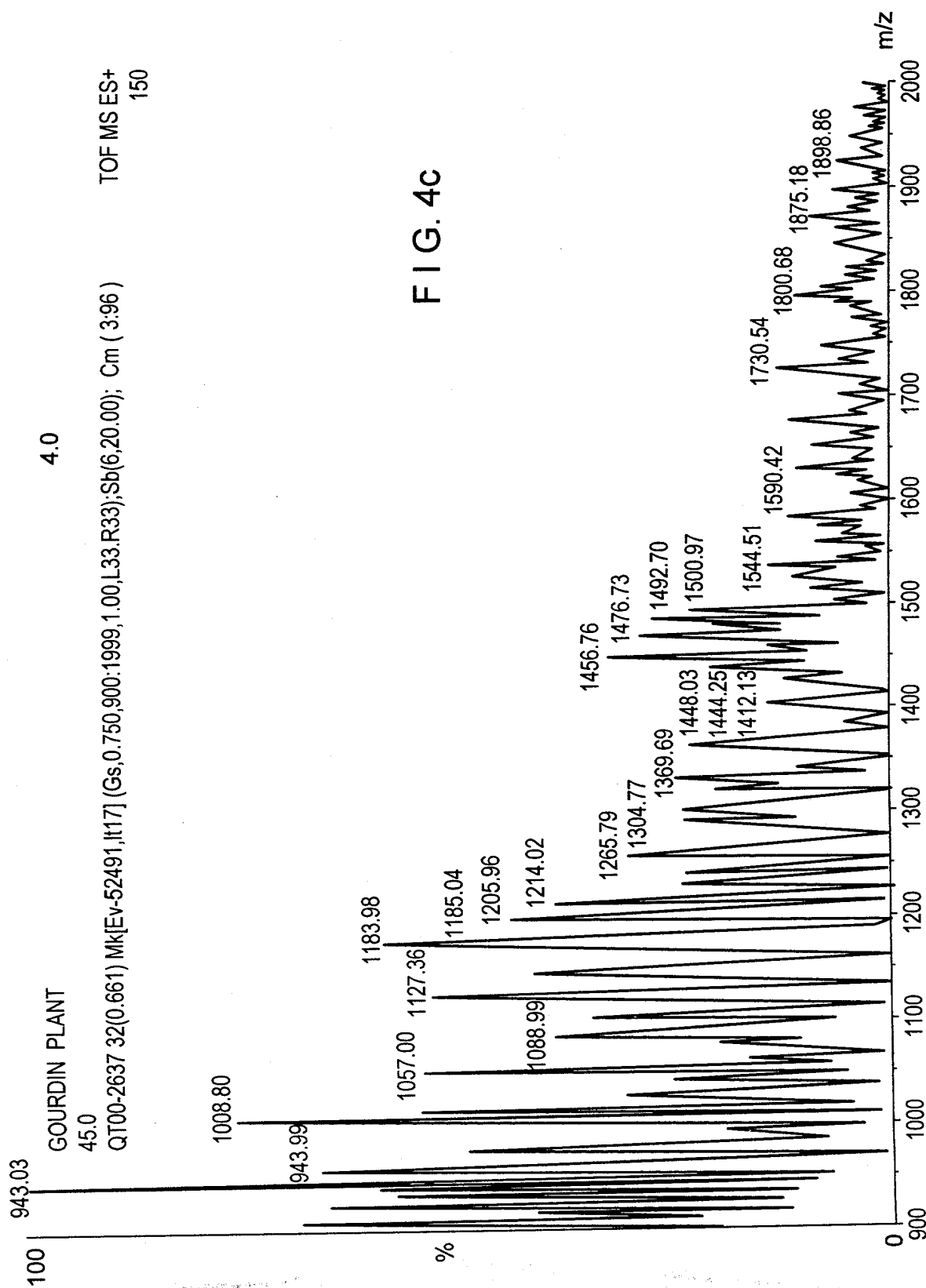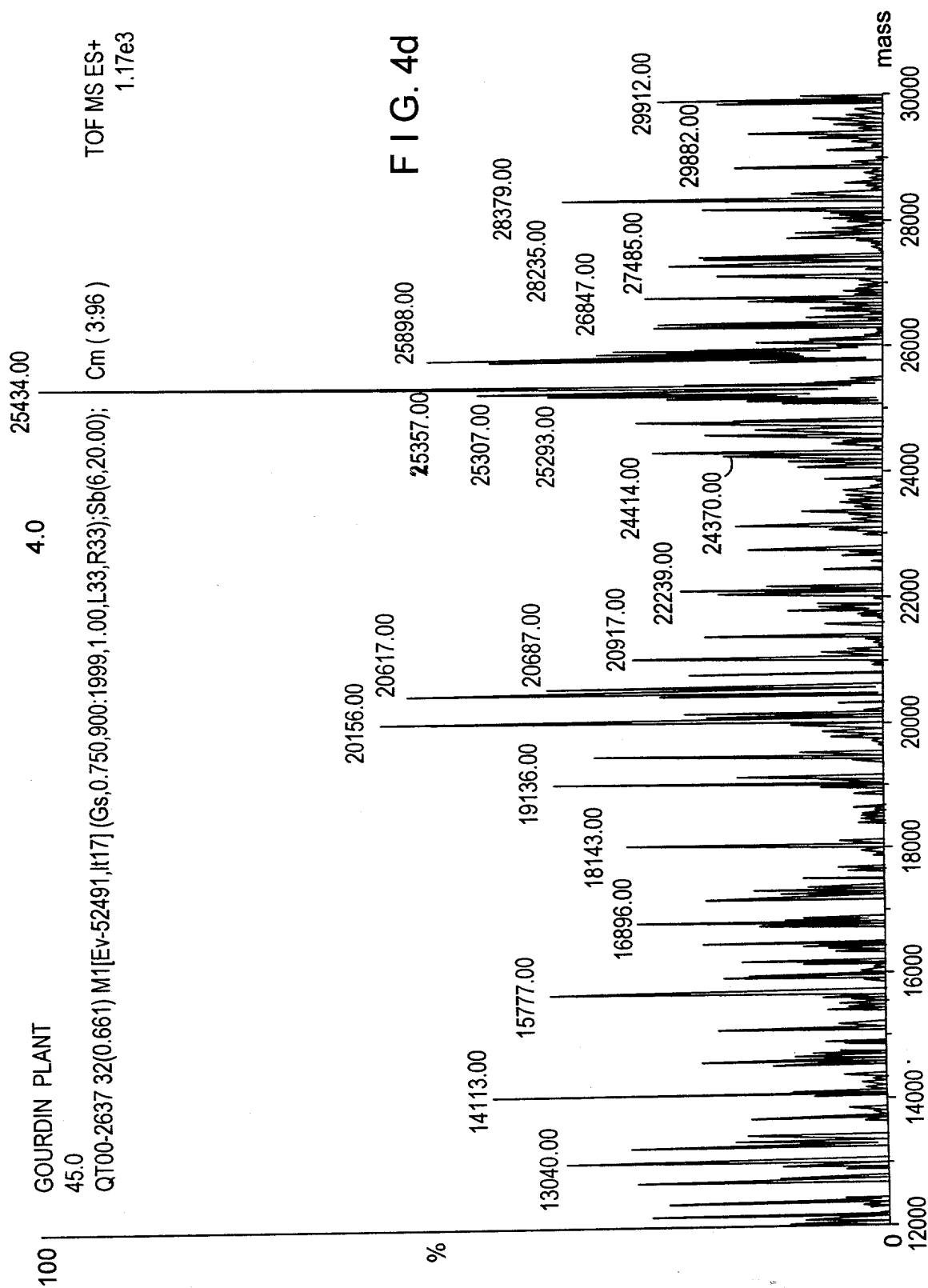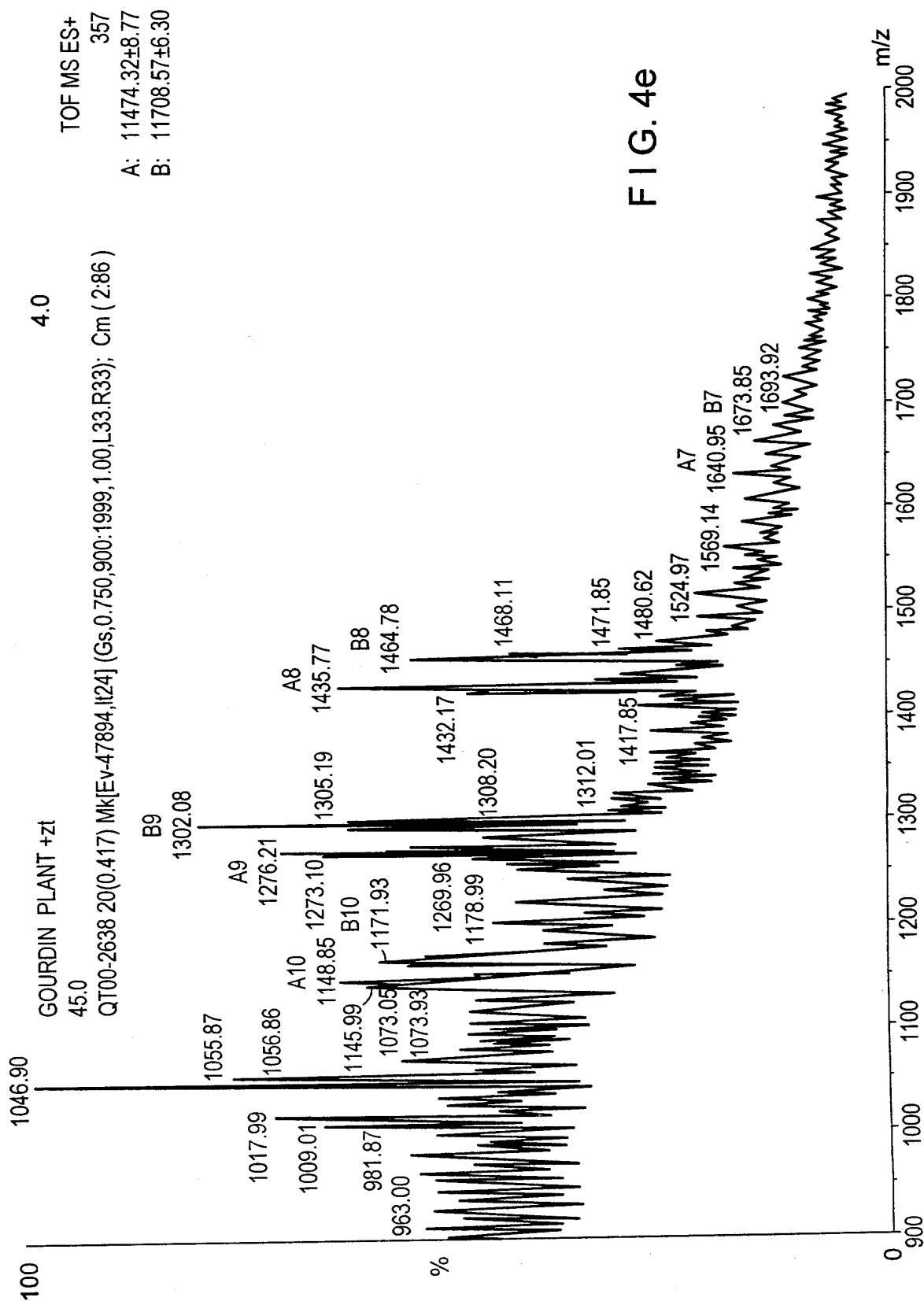
INTERFACE 01 0-68 Min  SCALE: 15 Mv Ch. A,  15 Mv Ch. B
AMINO ACID ANALYSI   PROCESSED: 11-22-2000 14:26:30,  SEGMENT 17,  CYCLE 936
RAW DATA SAVED IN FILE K : AAA936.PTS  SECOND CHANNEL STORED IN K : BAA936.PTS

## EXTERNAL STANDARD TABLE

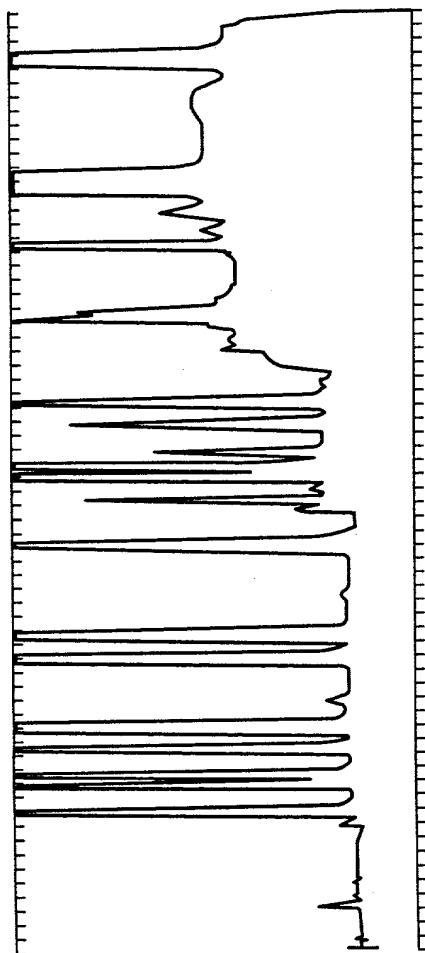*********************** 11-22-2000  14 : 26 : 30   Version 4.1 ***********************   Data File: K:AAA936

Sample Name: amino acid analysis

Date: 11-22-2000  14 : 26 : 30   Method: F:REBECKA                    11-22-2000   13 : 54 : 21   # 457

Interface: 0          Cycle #: 936       Operator jmc      Channel #: 0      Vial #: N.A.

Starting Peak Width: 21    Threshold: 5     Area Threshold: 500

*********************************************************************************

Starting Delay:        0.00                                    Ending retention time:      68.00

Area reject:           5000                                    One sample per:          2.002 sec.

Amount injected:       1.00                                    Dilution factor:             1.00

Sample weight:         1.000000

SEE  FIG. 5a2

## F I G. 5a1

SEE FIG. 5a1

| PEAK NUM | RET TIME | PEAK NAME | CONCENTRATION in nmoles | NORMALIZED CONC | AREA | HEIGHT | AREA/HEIGHT | BL | REF PEAK | % DELTA RET TIME | CONC/AREA |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 2.936 | | | 0.1504% | 20695 | 1550 | 13.4 | 1 | 6 | -1.592 | 3.4373E-06 |
| 2 | 8.609 | | | 0.0856% | 9566 | 096 | 13.7 | 1 | 6 | 0 | 4.28185E-06 |
| 3 | 9.543 | asx | 3.6346 | 7.6853% | 1019304 | 61489 | 16.6 | 1 | 6 | .5811 | 3.5658E-06 |
| 4 | 11.378 | thr | 1.1549 | 2.4420% | 314916 | 15245 | 20.7 | 2 | 6 | .1132 | 3.6674E-06 |
| 5 | 12.112 | ser | 2.0456 | 4.3254% | 595007 | 27668 | 21.5 | 2 | 6 | 0 | 3.4380E-06 |
| 6 | 14.081 | int. std. | 1.0397 | 2.1985% | 576309 | 23599 | 24.4 | 2 | 6 | 0 | 1.0041E-06 |
| 7 | 15.649 | glx | 6.6195 | 13.9567% | 1959672 | 71617 | 27.4 | 2 | 6 | .1667 | 3.3779E-06 |
| 8 | 17.651 | pro+ cys | 2.1133 | 6.1414% | 28161 | 809 | 34.8 | 2 | 6 | -.2854 | 1.0314E-04 |
| 9 | 20.554 | gly | 3.4509 | 7.2968% | 1098728 | 36599 | 30.0 | 2 | 9 | 0 | 3.1408E-06 |
| 10 | 22.256 | ala | 2.8168 | 5.9961% | 801412 | 25276 | 31.7 | 2 | 9 | 0 | 3.5248E-06 |
| 11 | 28.996 | val | 2.6160 | 5.4358% | 783543 | 16490 | 42.7 | 1 | 9 | 0 | 3.6541E-06 |
| 12 | 32.299 | set | 0.5625 | 1.1894% | 157161 | 8772 | 17.9 | 1 | 16 | .0101 | 3.5792E-06 |
| 13 | 33.166 | | 0.0000 | 0.0000% | 10132 | 523 | 19.4 | 1 | 16 | | 0.0000E+00 |
| 14 | 33.967 | ileu | 1.8404 | 3.8914% | 535119 | 23330 | 22.9 | 2 | 16 | -.0931 | 3.4392E-06 |
| 15 | 34.735 | leu | 3.1701 | 6.7031% | 953284 | 38035 | 25.1 | 2 | 16 | 0 | 3.3255E-06 |
| 16 | 35.902 | nl-std. | 6.2739 | 0.5791% | 163238 | 6196 | 26.3 | 2 | 16 | 0 | 1.6777E-06 |
| 17 | 37.871 | tyr | 1.0645 | 2.2508% | 290327 | 9412 | 30.8 | 1 | 16 | 0 | 3.6666E-06 |
| 18 | 39.473 | phe | 1.6115 | 3.4075% | 408260 | 12881 | 31.7 | 1 | 16 | 0 | 3.9472E-06 |
| 19 | 45.479 | his | 1.2110 | 2.6711% | 203562 | 8185 | 24.9 | 2 | 16 | 0 | |
| 20 | 46.013 | | 0.0000 | 0.0000% | 154147 | 5442 | 26.3 | 2 | 16 | 0 | 0.0000E+00 |
| 21 | 50.751 | lys | 1.2451 | 2.6327% | 385456 | 13267 | 29.1 | 2 | 16 | 0 | 3.2302E-06 |
| 22 | 51.885 | | | 0.3929% | 32441 | 913 | 35.5 | 2 | 16 | 0 | 5.7275E-06 |
| 23 | 53.287 | | 0.0000 | 0.0000% | 102408 | 2246 | 46.6 | 2 | 16 | 0 | 0.0000E+00 |
| 24 | 55.355 | NH4 | 6.1666 | 13.0391% | 3568874 | 61870 | 57.7 | 2 | 16 | 0 | 1.7279E-06 |
| 25 | 64.197 | arg | 3.5602 | 7.5279% | 1016938 | 22156 | 45.9 | 1 | 16 | 0 | 3.5009E-06 |

TOTAL AMOUNT: 47.2934

FIG. 5a2

AREAS, TIMES, AND HEIGHTS STORED IN : K: AAA936.ATB
DATA FILE = K: AAA936.PTS    PRINTED ON 11-22-2000  AT  14:27:06
START TIME :  0.00 min.   STOP TIME :  68.00 min.   OFFSET :   0 mv
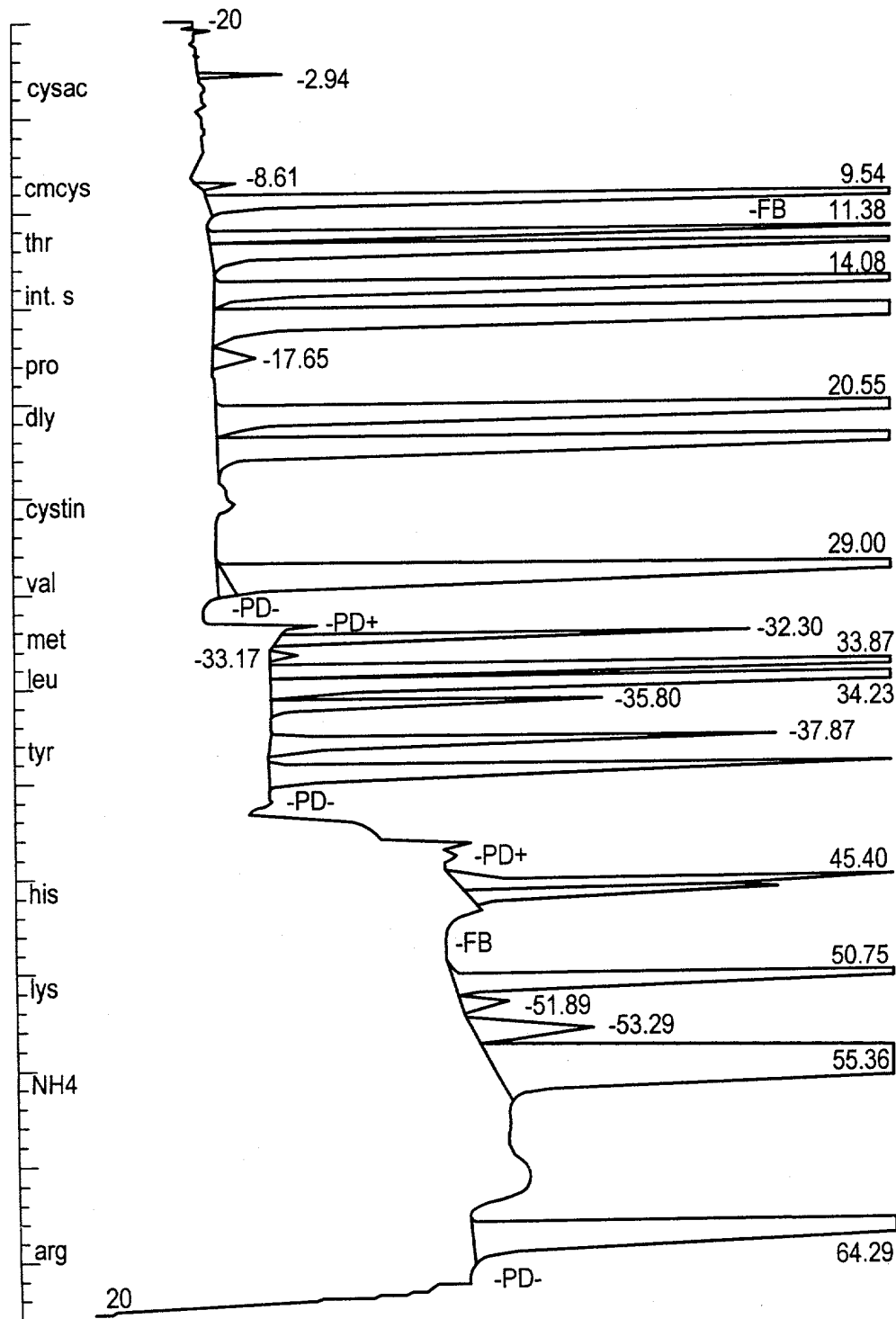FULL RANGE :   15  millivolts



F I G. 5b

## EXTERNAL STANDARD TABLE

******************* 11-22-2000  14:28:43  Version 4.1 ******************************

Sample Name: amino acid analysis

Data File: K:BAA936

Date: 11-22-2000  14:26:30  Method: F:REBECKA          11-22-2000  13:55:21  # 257

Interface: 0          Cycle #: 936          Operator jmc          Channel #: 1          Vial #: N.A.

Starting Peak Width: 21   Threshold: .5   Area Threshold: 500

***************************************************************************

| Starting Delay: | 0.00 | | Ending retention time: | 68.00 |
| Area reject: | 5000 | | One sample per: | 2.002 sec. |
| Amount injected: | 1.00 | | Dilution factor: | 1.00 |
| Sample weight: | 1.000000 | | | |

| PEAK NUM | RET TIME | PEAK NAME | CONCENTRATION in nmoles | NORMALIZED CONC | AREA | HEIGHT | AREA/ HEIGHT | BL | REF PEAK | % DELTA RET TIME | CONC/ AREA |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 8.775 | | 0.0000 | 0.0000% | 5143 | 286 | 18.0 | 1 | | | 0.0000E+00 |
| 2 | 9.510 | | 0.0000 | 0.0000% | 129394 | 7707 | 16.8 | 1 | | | 0.0000E+00 |
| 3 | 11.345 | | 0.0000 | 0.0000% | 24969 | 1171 | 21.3 | 2 | | | 0.0000E+00 |
| 4 | 12.079 | | 0.0000 | 0.0000% | 59106 | 2389 | 24.7 | 2 | | | 0.0000E+00 |
| 5 | 14.047 | | 0.0000 | 0.0000% | 47121 | 1978 | 23.8 | 1 | | | 0.0000E+00 |
| 6 | 15.616 | glx | 6.2317 | 74.6757% | 375516 | 13802 | 27.2 | 1 | 7 | .2393 | 1.6595E-05 |
| 7 | 17.651 | pro+cys | (2.1133) | 25.3244% | 199944 | 6665 | 30.0 | 1 | 7 | 0 | 1.0570E-05 |
| 8 | 20.554 | | 0.0000 | 0.0000% | 83682 | 2753 | 30.4 | 1 | | | 0.0000E+00 |
| 9 | 22.222 | | 0.0000 | 0.0000% | 67237 | 2027 | 33.2 | 1 | | | 0.0000E+00 |

TOTAL AMOUNT:          8.3451

SEE FIG. 5c2

## FIG. 5c1

SEE FIG. 5c1

AREAS, TIMES, AND HEIGHTS STORED IN : K: BAA936.ATB
DATA FILE = K: BAA936.PTS    PRINTED ON 11-22-2000  AT  14:28:59
START TIME :  0.00 min.    STOP TIME :  68.00 min.    OFFSET : -95 mv
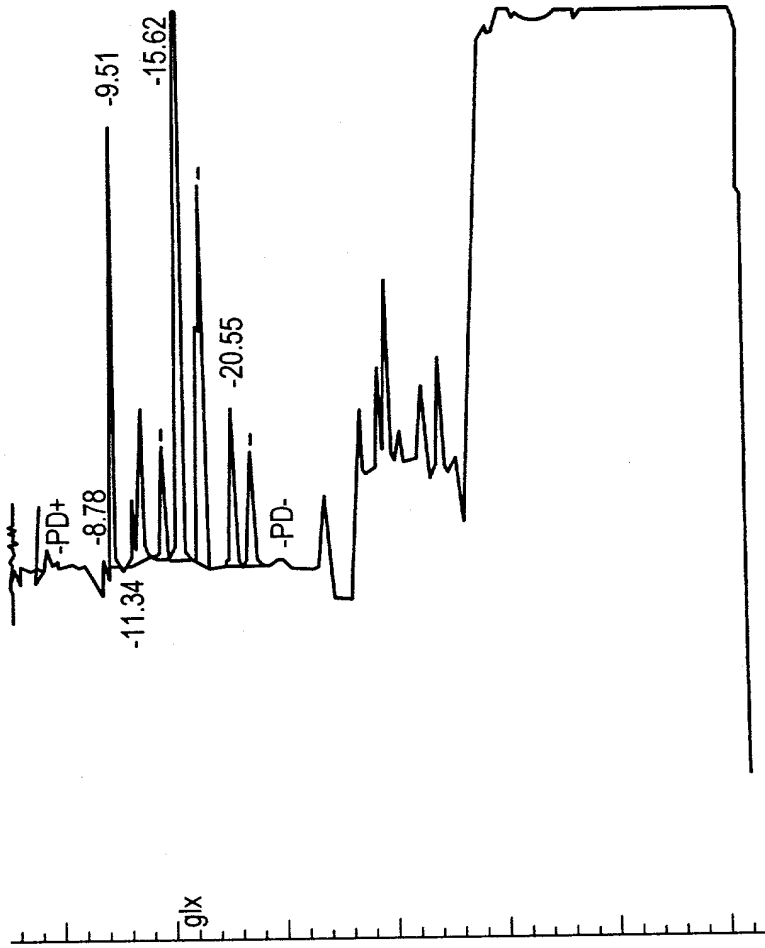FULL RANGE :   15  millivolts

F I G. 5c2